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1600

RAW SEQUENCE LISTING

DATE: 06/03/2003

PATENT APPLICATION: US/09/308,829

TIME: 11:02:16

Input Set : A:\Sequence listing.txt

Output Set: N:\CRF4\06032003\I308829.raw

3 <110> APPLICANT: Schlievert, Patrick M.
 4 Ohlendorf, Douglas
 5 Mitchell, David T.
 6 Gahr, Pamala J.
 8 <120> TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN C AND METHODS OF USE
 10 <130> FILE REFERENCE: 600.347USWO
 12 <140> CURRENT APPLICATION NUMBER: US 09/308,829
 13 <141> CURRENT FILING DATE: 1999-07-14
 15 <150> PRIOR APPLICATION NUMBER: PCT/US97/22125
 16 <151> PRIOR FILING DATE: 1997-12-05
 18 <150> PRIOR APPLICATION NUMBER: US 60/033,251
 19 <151> PRIOR FILING DATE: 1996-12-06
 21 <160> NUMBER OF SEQ ID NOS: 2
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 936
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Streptococcus pyogenes
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (154)..(858)
 33 <223> OTHER INFORMATION:

ENTERED

W--> 36 <400> 1

37	caaccttgac tatTTaaatg gaactgccac tcctaaaaaac taaaatataa atacatttat	60
39	aaaatttcta aataaacaga aatctgattt ttaactactt actgctattt catgtattct	120
41	cgtacgagta atacatttaa ttaaggagaaa aaa atg aaa aag att aac atc atc	174
42		
43		
45	aaa ata gtt ttc ata att aca gtc ata ctg att tct act tat ttc acc	222
46	Lys Ile Val Phe Ile Ile Thr Val Ile Leu Ile Ser Thr Tyr Phe Thr	
47	10 15 20	
49	tat cat caa agt gac tct aag aaa gac att tcg aat gtt aaa agt gat	270
50	Tyr His Gln Ser Asp Ser Lys Lys Asp Ile Ser Asn Val Lys Ser Asp	
51	25 30 35	
53	tta ctt tat gca tac act ata act cct tat gat tat aaa gat tgc agg	318
54	Leu Leu Tyr Ala Tyr Thr Ile Thr Pro Tyr Asp Tyr Lys Asp Cys Arg	
55	40 45 50 55	
57	gta aat ttt tca acg aca cac aca tta aac att gat act caa aaa tat	366
58	Val Asn Phe Ser Thr Thr His Thr Leu Asn Ile Asp Thr Gln Lys Tyr	
59	60 65 70	
61	aga ggg aaa gac tat tat att agt tcc gaa atg tct tat gag gcc tct	414
62	Arg Gly Lys Asp Tyr Tyr Ile Ser Ser Glu Met Ser Tyr Glu Ala Ser	
63	75 80 85	

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140          100          105          110
143 Ile Tyr Gly Gly Ile Thr Pro Ala Gln Asn Asn Lys Val Asn His Lys
144          115          120          125
147 Leu Leu Gly Asn Leu Phe Ile Ser Gly Glu Ser Gln Gln Asn Leu Asn
148          130          135          140
151 Asn Lys Ile Ile Leu Glu Lys Asp Ile Val Thr Phe Gln Glu Ile Asp
152 145          150          155          160
155 Phe Lys Ile Arg Lys Tyr Leu Met Asp Asn Tyr Lys Ile Tyr Asp Ala
156          165          170          175
159 Thr Ser Pro Tyr Val Ser Gly Arg Ile Glu Ile Gly Thr Lys Asp Gly
160          180          185          190
163 Lys His Glu Gln Ile Asp Leu Phe Asp Ser Pro Asn Glu Gly Thr Arg
164          195          200          205
167 Ser Asp Ile Phe Ala Lys Tyr Lys Asp Asn Arg Ile Ile Asn Met Lys
168          210          215          220
171 Asn Phe Ser His Phe Asp Ile Tyr Leu Glu Lys
172 225          230          235

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VERIFICATION SUMMARY

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L:36 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:33



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